

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising:
 - (a) a first nucleotide sequence encoding a first polypeptide comprising at least 100 amino acids, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4 have at least 70% identity based on the Clustal alignment method,
 - (b) a second nucleotide sequence encoding a second polypeptide comprising at least 150 amino acids, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:12 have at least 70% identity based on the Clustal alignment method,
 - (c) a third nucleotide sequence encoding a third polypeptide comprising at least 250 amino acids, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8 have at least 70% identity based on the Clustal alignment method,
 - (d) a fourth nucleotide sequence encoding a fourth polypeptide comprising at least 300 amino acids, wherein the amino acid sequence of the fourth polypeptide and the amino acid sequence of SEQ ID NO:10 have at least 80% identity based on the Clustal alignment method, or
 - (e) the complement of the first, second, third, or fourth nucleotide sequence, wherein the complement and the first, second, third, or fourth nucleotide sequence contain the same number of nucleotides and are 100% complementary.
2. The polynucleotide of Claim 1, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4 have at least 80% identity based on the Clustal alignment method, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:12 have at least 80% identity based on the Clustal alignment method, and wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8 have at least 80% identity based on the Clustal alignment method.
3. The polynucleotide of Claim 1, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4 have at least 85% identity based on the Clustal alignment method, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:12 have at least 85% identity based on the Clustal alignment method, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8 have at least 85% identity based on the Clustal alignment method, and wherein the amino acid

sequence of the fourth polypeptide and the amino acid sequence of SEQ ID NO:10 have at least 85% identity based on the Clustal alignment method.

4. The polynucleotide of Claim 1, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4 have at least 5 90% identity based on the Clustal alignment method, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:12 have at least 90% identity based on the Clustal alignment method, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8 have at least 90% identity based on the Clustal alignment method, and wherein the amino acid 10 sequence of the fourth polypeptide and the amino acid sequence of SEQ ID NO:10 have at least 90% identity based on the Clustal alignment method.

5. The polynucleotide of Claim 1, wherein the amino acid sequence of the first polypeptide and the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4 have at least 15 95% identity based on the Clustal alignment method, wherein the amino acid sequence of the second polypeptide and the amino acid sequence of SEQ ID NO:12 have at least 95% identity based on the Clustal alignment method, wherein the amino acid sequence of the third polypeptide and the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8 have at least 95% identity based on the Clustal alignment method, and wherein the amino acid 20 sequence of the fourth polypeptide and the amino acid sequence of SEQ ID NO:10 have at least 95% identity based on the Clustal alignment method.

6. The isolated polynucleotide of Claim 1, wherein the first polypeptide comprises the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4, wherein the second polypeptide comprises the amino acid sequence of SEQ ID NO:12, wherein the third polypeptide comprises the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8, and wherein the 25 fourth polypeptide comprises the amino acid sequence of SEQ ID NO:10.

7. The isolated polynucleotide of Claim 1, wherein the first nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:3, wherein the second nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:11, wherein the third nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:5 or SEQ ID NO:7, 30 and wherein the fourth nucleotide sequence comprises the nucleotide sequence of SEQ ID NO:9.

8. The isolated polynucleotide of Claim 1, wherein the first, second, third, and fourth polypeptides are SPF1-related transcription factors.

9. A chimeric gene comprising the polynucleotide of any of Claims 1-8 operably 35 linked to a regulatory sequence.

10. A vector comprising the polynucleotide of any of Claims 1-8.

11. An isolated polynucleotide fragment comprising a nucleotide sequence comprised by the polynucleotide of any of Claims 1-8, wherein the nucleotide sequence contains at least 30 nucleotides.

12. The fragment of Claim 11, wherein the nucleotide sequence contains at least

5 40 nucleotides.

13. The fragment of Claim 11, wherein the nucleotide sequence contains at least 60 nucleotides.

14. An isolated polypeptide comprising:

10 (a) a first amino acid sequence comprising at least 100 amino acids, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4 have at least 70% identity based on the Clustal alignment method,

15 (b) a second amino acid sequence comprising at least 150 amino acids, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:12 have at least 70% identity based on the Clustal alignment method,

(c) a third amino acid sequence comprising at least 250 amino acids, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8 have at least 70% identity based on the Clustal alignment method, or

20 (d) a fourth amino acid sequence comprising at least 300 amino acids, wherein the fourth amino acid sequence and the amino acid sequence of SEQ ID NO:10 have at least 80% identity based on the Clustal alignment method.

15. The polypeptide of Claim 14, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4 have at least 80% identity based on 25 the Clustal alignment method, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:12 have at least 80% identity based on the Clustal alignment method, and wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8 have at least 80% identity based on the Clustal alignment method.

16. The polypeptide of Claim 14, wherein the first amino acid sequence and the

30 amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4 have at least 85% identity based on the Clustal alignment method, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:12 have at least 85% identity based on the Clustal alignment method, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8 have at least 85% identity based on the Clustal alignment method, 35 and wherein the fourth amino acid sequence and the amino acid sequence of SEQ ID NO:10 have at least 85% identity based on the Clustal alignment method.

17. The polypeptide of Claim 14, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4 have at least 90% identity based on the Clustal alignment method, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:12 have at least 90% identity based on the Clustal alignment
5 method, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8 have at least 90% identity based on the Clustal alignment method, and wherein the fourth amino acid sequence and the amino acid sequence of SEQ ID NO:10 have at least 90% identity based on the Clustal alignment method.

18. The polypeptide of Claim 14, wherein the first amino acid sequence and the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4 have at least 95% identity based on the Clustal alignment method, wherein the second amino acid sequence and the amino acid sequence of SEQ ID NO:12 have at least 95% identity based on the Clustal alignment method, wherein the third amino acid sequence and the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8 have at least 95% identity based on the Clustal alignment method,
10 and wherein the fourth amino acid sequence and the amino acid sequence of SEQ ID NO:10 have at least 95% identity based on the Clustal alignment method.

19. The polypeptide of Claim 14, wherein the first amino acid sequence comprises the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4, wherein the second amino acid sequence comprises the amino acid sequence of SEQ ID NO:12, wherein the third amino
20 acid sequence comprises the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:8, and wherein the fourth amino acid sequence comprises the amino acid sequence of SEQ ID NO:10.

20. The polypeptide of Claim 14, wherein the polypeptide is an SPF1-related transcription factor.

25 21. A method for transforming a cell comprising introducing the polynucleotide of any of Claims 1-8 into a cell.

22. A cell comprising the chimeric gene of Claim 9.

23. A method for producing a transgenic plant comprising transforming a plant cell with the polynucleotide of any of Claims 1-8 and regenerating a plant from the transformed
30 plant cell.

24. A plant comprising the chimeric gene of Claim 9.

25. A seed comprising the chimeric gene of Claim 9.